



0590  
0829

## **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/828,995A  
Source: O/PE  
Date Processed by STIC: 9/13/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/828,995A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length  
Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9      Use of n's or Xaa's  
    (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>  
Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/828,995A

DATE: 09/13/2001  
 TIME: 11:05:09

Input Set : A:\A1-71.app  
 Output Set: N:\CRF3\09132001\I828995A.raw

*pp 1-2*  
 Does Not Comply  
 Corrected Diskette Needed

3 <110> APPLICANT: McCall, Catherine A.  
 4 Tang, Liang  
 5 Heska Corporation  
 7 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND  
 8 CANINE IL-13 RECEPTORS  
 10 <130> FILE REFERENCE: AL-7  
 12 <140> CURRENT APPLICATION NUMBER: 09/828,995A  
 13 <141> CURRENT FILING DATE: 2001-04-09  
 15 <150> PRIOR APPLICATION NUMBER: 60/195,659  
 16 <151> PRIOR FILING DATE: 2000-04-07  
 18 <150> PRIOR APPLICATION NUMBER: 60/195,874  
 19 <151> PRIOR FILING DATE: 2000-04-07  
 21 <160> NUMBER OF SEQ ID NOS: 104  
 23 <170> SOFTWARE: PatentIn Ver. 2.1

# ERRORED SEQUENCES

1358 <210> SEQ ID NO: 26  
 1359 <211> LENGTH: 239  
 1360 <212> TYPE: PRT  
 1361 <213> ORGANISM: Canis familiaris  
 1363 <400> SEQUENCE: 26  
 1364 Met Ser Ser Asp Met Ala Trp Ser Pro Leu Leu Leu Thr Leu Leu Ala  
 1365 1 5 10 15  
 1367 His Cys Thr Gly Ser Trp Ala Gln Ala Val Leu Asn Gln Pro Ala Ser  
 1368 20 25 30  
 1370 Val Ser Gly Ala Leu Gly Gln Lys Val Thr Ile Ser Cys Ser Gly Asp  
 1371 35 40 45  
 1373 Thr Asn Asp Ile Asp Ile Phe Gly Val Asn Trp Tyr Gln Gln Leu Pro  
 1374 50 55 60  
 1376 Gly Lys Ala Pro Thr Val Leu Val Asp Ser Asp Gly Asp Arg Pro Ser  
 1377 65 70 75 80  
 1379 Gly Val Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Ser Gly Thr  
 1380 85 90 95  
 1382 Leu Thr Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys  
 1383 100 105 110  
 1385 Gln Ser Val Asp Ser Thr Leu Gly Val Tyr Val Phe Gly Ser Gly Thr  
 1386 115 120 125  
 1388 Gln Leu Thr Val Leu Gly Gln Pro Lys Ala Ser Pro Ser Val Thr Leu  
 1389 130 135 140  
 E--> 1391 Phe Pro Xaa Xaa Xaa Glu Glu Leu Gly Ala Asn Lys Ala Thr Leu Val  
 1392 145 150 155 160  
 E--> 1394 Cys Leu Ile Ser Asp Phe Tyr Pro Xaa Gly Val Thr Val Ala Trp Lys  
 1395 165 170 175  
 1397 Ala Asp Gly Ser Pro Val Thr Gln Gly Val Glu Thr Thr Lys Pro Ser  
 1398 180 185 190

*See item 9 on  
 Error Summary  
 Sheet*

## RAW SEQUENCE LISTING

DATE: 09/13/2001

PATENT APPLICATION: US/09/828,995A

TIME: 11:05:09

Input Set : A:\A1-71.app

Output Set: N:\CRF3\09132001\I828995A.raw

1400 Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr  
1401           195                           200                           205  
1403 Pro Asp Lys Trp Lys Ser His Ser Ser Phe Ser Cys Leu Val Thr His  
1404           210                           215                           220  
1406 Glu Gly Ser Pro Val Glu Lys Lys Val Ala Pro Ala Lys Cys Ser  
1407 225                           230                           235

fwd →

Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.

## VERIFICATION SUMMARY

DATE: 09/13/2001

PATENT APPLICATION: US/09/828,995A

TIME: 11:05:11

Input Set : A:\A1-71.app

Output Set: N:\CRF3\09132001\I828995A.raw

L:703 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:959 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:1324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:1332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:1391 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26  
M:340 Repeated in SeqNo=26  
L:1429 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:1506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:1508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:1574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:1575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:2251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
L:2363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48  
L:2865 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57  
L:2935 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59  
L:3073 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60  
L:3172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62  
L:4904 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83  
L:4937 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84  
L:4965 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85  
L:4993 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86  
L:5026 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87  
L:5049 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:88